coding sequence from a host bacterium for bacteriophage 77. Target sequences are described herein by reference to sequence source sites. The sequence encoding the target preferably corresponds to a *S. aureus* nucleic acid sequence available from numerous sources including *S. aureus* sequences deposited in GenBank, *S. aureus* sequences found in European Patent Application NO: 97100110.7 to Human Genome Sciences, Inc. filed January 7, 1997, *S. aureus* sequences available from TIGR at the Web site for which the remainder of the address after www is tigr.org/tdb/mdb/mdb.html, and *S. aureus* sequences available from the Oklahoma University *S. aureus* sequencing project at theWeb site for which the remainder of the address following www is genome.ou.edu/staph_new.html.

Replacement paragraph at p.25, line 23 to p.26, line 2.

The present invention is based on the identification of naturally-occurring DNA sequence elements encoding RNA or proteins with anti-microbial activity. Bacteriophages or phages, are viruses that infect and kill bacteria. They are natural enemies of bacteria and, over the course of evolution have perfected enzymes (products of DNA sequences) which enable them to infect a host bacterium, replicate their genetic material, usurp host metabolism, and ultimately kill their host. The scientific literature documents well the fact that many known bacteria have a large number of such bacteriophages than can infect and kill them (for example, see the ATCC bacteriophage collection at the Web site atcc.org) (Ackermann and DuBow, 1987). Although we know that many bacteriophages encode proteins which can significantly alter their host's metabolism, determination of the killing potential of a given bacteriophage gene product can only be assessed by expressing the gene product in the target bacterial strain.

Replacement paragraph at p.45, lines 6-15.

A software program was developed and used on the assembled sequence of bacteriophage 77 to identify all putative ORFs larger than 33 codons. Other ORF identification software can also be utilized, preferably programs which allow alternative start codons. The software scans

the primary nucleotide sequence starting at nucleotide #1 for an appropriate start codon. Three possible selections can be made for defining the nature of the start codon: I) selection of ATG, II) selection of ATG or GTG, and III) selection of either ATG, GTG, TTG, CTG, ATT, ATC, and ATA. This latter initiation codon set corresponds to the one reported by the NCBI (at the Web site ncbi.nlm.nih.gov/htbin-post/Taxonomy/wprintgc?mode=c) for the bacterial genetic code.

Replacement paragraph at p.45, line 24 to p.46, line 6.

Sequence homology (BLAST) searches for each ORF are then carried out using an implementation of BLAST programs, although any of a variety of different sequence comparison and matching programs can be utilized as known to those skilled in the art. Downloaded public databases used for sequence analysis include:
i) non-redundant GenBank (at the ftp site ncbi.nlm.nih.gov/blast/db/nr.Z),
ii) Swissprot (at the ftp site ncbi.nlm.nih.gov/blast/db/swissprot.Z);
iii) vector (at the ftp site ncbi.nlm.nih.gov/blast/db/vector.Z);
iv) pdbaa databases (at the ftp site ncbi.nlm.nih.gov/blast/db/pdbaa.Z);
v) *Staphylococcus aureus* NCTC 8325 (at the ftp site ftp.genome.ou.edu/pub/staph/staph-1k.fa);
vi) *Streptococcus pyogenes* (at the ftp site ftp.genome.ou.edu/pub/strep/strep-1k.fa);
vii) *Streptococcus pneumoniae* (at the ftp site ftp.tigr.org/pub/data/s_pneumoniae/gsp.contigs.112197.Z);
viii) *Mycobacterium tuberculosis* CSU#9 (at the ftp site ftp.tigr.org/pub/data/m_tuberculosis/TB_091097.Z) and ix) *Pseudomonas aeruginosa* (at the Web site genome.washington.edu/pseudo/data.html).

In the claims:

Cancel claims 10, 57, 58, and 65-67 without prejudice to prosecution of the subject matter in this or another appropriate application.